Transcriptome profiling of endothelial cells during infections with high and low densities of Candida albicans cells.

ABSTRACT

Systemic infections of Candida albicans, the most prevalent fungal pathogen in humans, are on the rise in recent years. However, the exact mode of pathogenesis of this fungus is still not well elucidated. Previous studies using C. albicans mutants locked into the yeast form via gene deletion found that this form was avirulent and did not induce significant differential expression of host genes in vitro. In this study, a high density of C. albicans was used to infect human umbilical vein endothelial cells (HUVEC), resulting in yeast-form infections, whilst a low density of C. albicans resulted in hyphae infections. Transcriptional profiling of HUVEC response to these infections showed that high densities of C. albicans induced a stronger, broader transcriptional response from HUVEC than low densities of C. albicans infection. Many of the genes that were significantly differentially expressed were involved in apoptosis and cell death. In addition, conditioned media from the high-density infections caused a significant reduction in HUVEC viability, suggesting that certain molecules released during C. albicans and HUVEC interactions were capable of causing cell death. This study has shown that C. albicans yeast-forms, at high densities, cannot be dismissed as avirulent, but instead could possibly contribute to C. albicans pathogenesis.

Keyword: Candida albicans; Yeast; Hyphae; Gene expression; Cell density; Endothelial cells.